

10/553124

SEQUENCE LISTING  
JC20 Rec'd PCT/PTO 14 OCT 2005

<110> TAISEI CORPORATION

<110> AJINOMOTO CO., INC.

<120> GENE THAT IMPARTS SALT STRESS TOLERANCE

<130> PH-2125-PCT

<150> JP2003-113194

<151> 2003-04-17

<150> JP2004-075932

<151> 2004-03-17

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1554

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (131)..(1222)

<400> 1

ggcacgagga ggcgcgccgc cggttgccag acactgccag tgcaacagag ccgcaaaacc 60

acacgcccc tcgcgcgctc acacagagag agacacacag atcgatcgag cggccggccg 120

gacggcgca gat gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg 169

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Ala

1

5

10

ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc 217

Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile

15

20

25

ggc acg cac acg gcg ctg cgc ctg ctg gag cag ggc tac ggc gtc acc 265

Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr

30

35

40

45

gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc 313

Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val

50

55

60

cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cgg 361

Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg

65

70

75

ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg 409

Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg

80

85

90

agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag 457

Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu  
95 100 105

agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc 505  
Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr  
110 115 120 125

atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg 553  
Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val  
130 135 140

tcc tcg tcg tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc 601  
Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys  
145 150 155

gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag 649  
Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys  
160 165 170

ctc atc ctg gag gag ttg gcg cgg gac tac cag cgc gcg gac ccg ggc 697  
Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly  
175 180 185

tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc 745  
Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser  
190 195 200 205

tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg 793  
3/21

Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu  
210 215 220

ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc 841  
Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val  
225 230 235

tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac 889  
Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr  
240 245 250

ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag 937  
Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys  
255 260 265

ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca 985  
Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr  
270 275 280 285

ggg cgc ggc aca tcc gtt ctc gag atg gtg gcg gcg ttc aag aag gca 1033  
Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala  
290 295 300

tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac 1081  
Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp  
305 310 315

gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctc gga 1129  
4/21

Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly

320                    325                    330

tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac 1177

Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn

335                    340                    345

tgg gcc aag aag aac ccc tat ggc tac tgc ggc act gcc .gaa aaa 1222

Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys

350                    355                    360

tagagcgcgt gcattaatca gatctctgga ctgaatttgt ccatgggtga tggttgtctc 1282

agacctatcg gtggaaagatg taacaaggtag agaccgctcg aatgtgccta gctacgaaag 1342

tttcgtacca tctcttttgt cataaacctca tgttagatggc cattttattt gaatttagcct 1402

tagccttcag gccccggcgtt gtttagccatt gcttgcatac gaggttaggtg gggtttggaaac 1462

tttggcgcc cttaacttc cattatcatc attcgacag acggcacagt tgccgagtga 1522

gccgttgaact gcttgtaaaa aaaaaaaaaaa aa 1554

<210> 2

〈211〉 364

〈212〉 PRT

<213> Seashore Paspalum

<400> 2

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Ala Gly Ala Ser

1 5 10 15

Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr His

20 25 30

Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp

35 40 45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile

50 55 60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu

65 70 75 80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp

85 90 95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala

100 105 110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu

115 120 125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser

130 135 140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp

145

150

155

160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu

165

170

175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile

180

185

190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu

195

200

205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile

210

215

220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His

225

230

235

240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val

245

250

255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp

260

265

270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly

275

280

285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys

290                    295                    300  
  
Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu  
305                    310                    315                    320  
  
Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala  
325                    330                    335  
  
Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys  
340                    345                    350  
  
Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys  
355                    360  
  
<210> 3  
  
<211> 24  
  
<212> DNA  
  
<213> Artificial Sequence  
  
  
<220>  
  
<223> Description of Artificial Sequence: synthetic oligonucleotide  
  
  
<400> 3  
  
ggtgcgacg actcctggag cccg                    24  
  
  
<210> 4  
  
<211> 24  
  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 4

ttgacaccag accaactggtaatg

24

<210> 5

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 5

tgccgtggc tccggcggt tcgccttcca cgagcaccac gagaagaagg aggaccacaa 60  
ggacgccgag gaggccggcg gcgagaagaa gcaccacttc ttccggctgat ccatctcacc 120  
atctccatct cccacccca tcgatccatt tgtgtggct ttaattccct gcgtgcattgc 180  
gtgttgtga ataaggggcc ggttccatct gtacgtacgt gtactccgag acctatcgac 240  
atgtgtgtgt gtgtacgtat acctgctgt tacatgatgg tcgttatatgc cactggacta 300  
tgtgtgtgtg caactctgtt ctgatttgct atatataag

339

<210> 6

<211> 497

<212> DNA

<213> Seashore Paspalum

<400> 6

tgcagggacc agtggactg ggccaagaag aaccctatg gctactgcgg cactgccgaa 60  
aaatagagcg cgtgcattaa tcagatctct ggactgaatt tgtccatggc tgatggttgt 120  
ctcagaccta tcggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180  
agtttcgtac catctctttt gtcataacct catgttagatg gtcattttat tggaaattagc 240  
cttagccttc aggccccggcg ctgttaaat ttgttttaca catggatttt ctcgctacgt 300  
gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca 360  
cgacggtgtgc tacgcccgtgt gttgttagtac tgtgaatatg atgtggtaat aacaataact 420  
tgcagtgaga cttcagcttt caaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 480  
aaaaaaaaaaa aaaaaaaaaaaa 497

497

<210> 7

<211> 396

<212> DNA

### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 7

ggccgctgtc cagggaccag tggaactggg ccaagaagaa cccctatggc tactgcggca 60  
ctgccgaaaa atagagcgcg tgcattaatc agatctctgg actgaatttg tccatggttg 120  
atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct 180  
agctacgaag ttctgttacca tctctcttgt cataacctca tgttagatggc cattttatttg 240  
gaatttagcct tagccttcag gcccggcgct gttaaaattt gttttacaca tggattttct 300  
cgctacgtgt gatacatatt gtgtctgtaa taatcctgtat cggagtttcc agtaataaaaa 360  
ccgatccacg acgggtggcta cgccctgtgt tgtagt 396

396

<210> 8

<211> 1540

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (110)..(1183)

<400> 8

ggcacgaggg agagatttagg aggaaatcga gttcatcctc cctccaccat cgccgatcat 60

agccttcctt tccccgatcg ccgatccgat ccacaagcaa gcagccagg atg gtt tct 118

Met Val Ser

1

gcg gtg ctt cgt acc atc ctt gtg acg ggc ggc gcc ggc tac atc ggc 166

Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly

5

10

15

agc cac acc gtg ctg ctg ctg cag cag gga ttc cgc gtc gtc gtc 214

Ser His Thr Val Leu Leu Leu Gln Gln Gly Phe Arg Val Val Val

20

25

30

35

gtc gac aac ctc gac aac gcc tcc gac gtc gcg ctc gcc cgc gtc gcg 262

Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala Arg Val Ala

40

45

50

cag ctc gca gca agc agc aac ggc ggc gcc gcc aac ctc gtc ttc cac 310  
Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu Val Phe His

55 60 65

aag gtt gac ctt cgc gac agg cac gcg ctg gag gac atc ttc tcc tcc 358  
Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile Phe Ser Ser

70 75 80

cac agg ttt gag gct gtg att cat ttt gct ggg ctc aaa gct gtt ggc 406  
His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly

85 90 95

gag agc gtg cag aag ccg ctg ctt tac tac gac aac aac ctc atc ggc 454  
Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly  
100 105 110 115

acc atc acc ctc ctc gag gtc atg gcc gca cat ggc tgc aag aag ctg 502  
Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu

120 125 130

gtg ttc tcg tca tct gca act gtc tat ggg tgg ccc aag gaa gtg cca 550  
Val Phe Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro

135 140 145

tgc acc gaa gaa ttc cct ctt tgc gcc acc aac ccc tat ggg cga acc 598  
Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr Gly Arg Thr

150 155 160

aag ctt gtg att gaa gat atc tgc cgc gac gtc cac cgt tca gac cct 646  
Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg Ser Asp Pro  
165 170 175

gat tgg aag atc ata ctg ctc agg tac ttc aac cct gtt ggt gct cat 694  
Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His  
180 185 190 195

cca agc gga cac atc ggt gaa gac ccc tct gga atc cca aac aac ctg 742  
Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu  
200 205 210

atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg agg cct cac ctc act 790  
Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr  
215 220 225

gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat 838  
Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp  
230 235 240

tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg 886  
Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly  
245 250 255

aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg 934  
Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu  
260 265 270 275

ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag 982

Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu

280

285

290

aag gtt tct ggc aag aaa atc cct ctg gtg ctt get ggg cga aga cct 1030

Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro

295

300

305

gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag 1078

Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu

310

315

320

ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag 1126

Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln

325

330

335

tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac 1174

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp

aac agc agc tgactgaaag caaatgcatg ctatgcata tagggagatc 1223

Asn Ser Ser

gaggcaggaga ccacttacca ctgtctatcc aagaagtgcg gtctcagaat accaccgtac 1283

gtatgcttac taaatagtcc gagggacggac ggacggatga tccatgtgtg gggcctcgta 1343

ttctcatttg tatagaggga cggagtagga gatccccagt cccatccatc cggcttattg 1403

ttgctaccgt caatccatgt ttaagaata aaccctatg catgtatgct tatcgatcta 1463

ctgtactagc taatttatata ggcatatgta tatttttag attcttatac aaaaaaaaaa 1523

aaaaaaaaaa aaaaaaaa 1540

<210> 9

<211> 358

<212> PRT

<213> Seashore Paspalum

<400> 9

Met Val Ser Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly

1

5

10

15

Tyr Ile Gly Ser His Thr Val Leu Leu Leu Gln Gln Gly Phe Arg

20

25

30

Val Val Val Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala

35

40

45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu

50

55

60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile

15/21

65 70 75 80

Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys

85 90 95

Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn

100 105 110

Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys

115 120 125

Lys Lys Leu Val Phe Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys

130 135 140

Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr

145 150 155 160

Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg

165 170 175

Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val

180 185 190

Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro

195 200 205

Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro

210 215 220

His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly  
225                    230                    235                    240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala  
245                    250                    255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val  
260                    265                    270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala  
275                    280                    285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly  
290                    295                    300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala  
305                    310                    315                    320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys  
325                    330                    335

Arg Asp Gln Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly  
340                    345                    350

Ser Pro Asp Asn Ser Ser  
355

<210> 10  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 10  
acagagccgc aaaaccacac 20

<210> 11  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 11  
ttcgttagcta ggcacatTCG agcggtg 27

<210> 12  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
18/21

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 12

gtcgtcgaca acttccacaa 20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 13

ttgttctcg tagtacatgtc 20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 14

atgaaaaagc ctgaactcac 20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 15

cgaacccgct cgtctggcta

20

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 16

gtggtcgaca acttccacaa

20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

20/21

<400> 17

ttgttctcgta catgta

17